

FIGURE 1

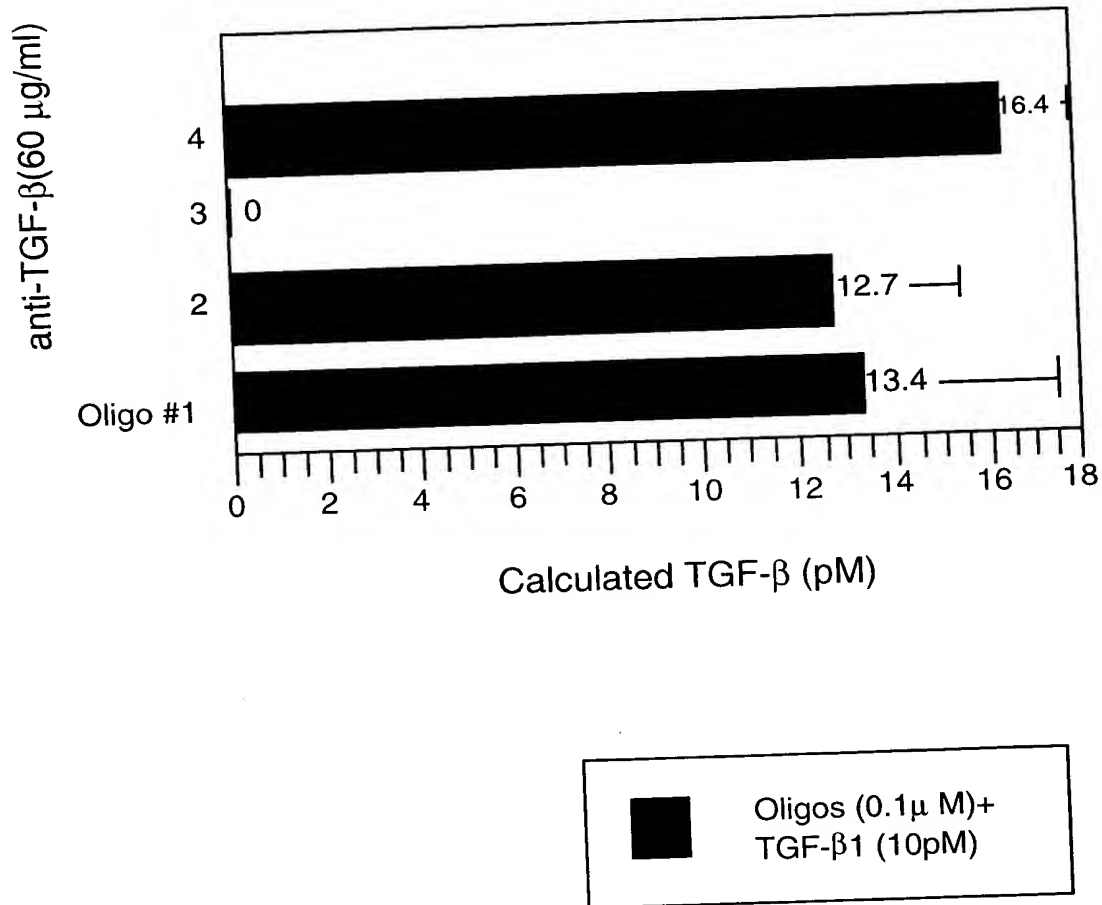
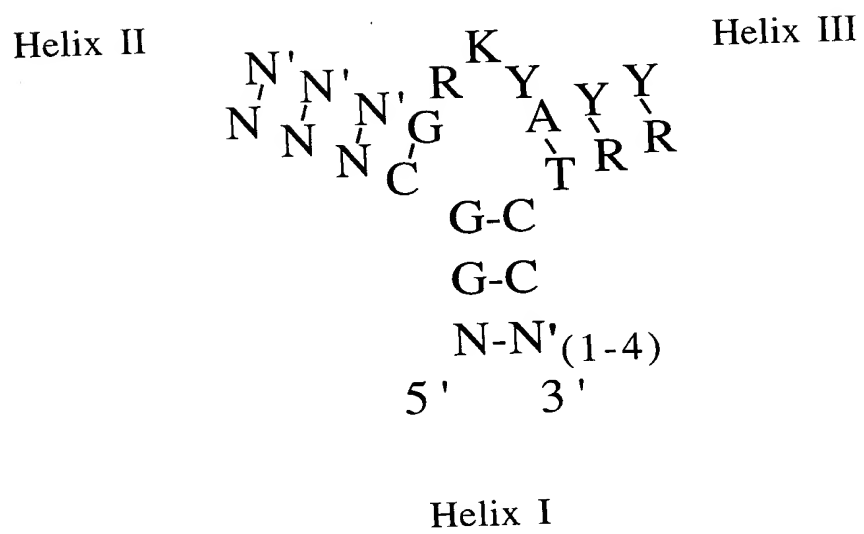


FIGURE 2



SEQ ID NO: 171

FIGURE 3

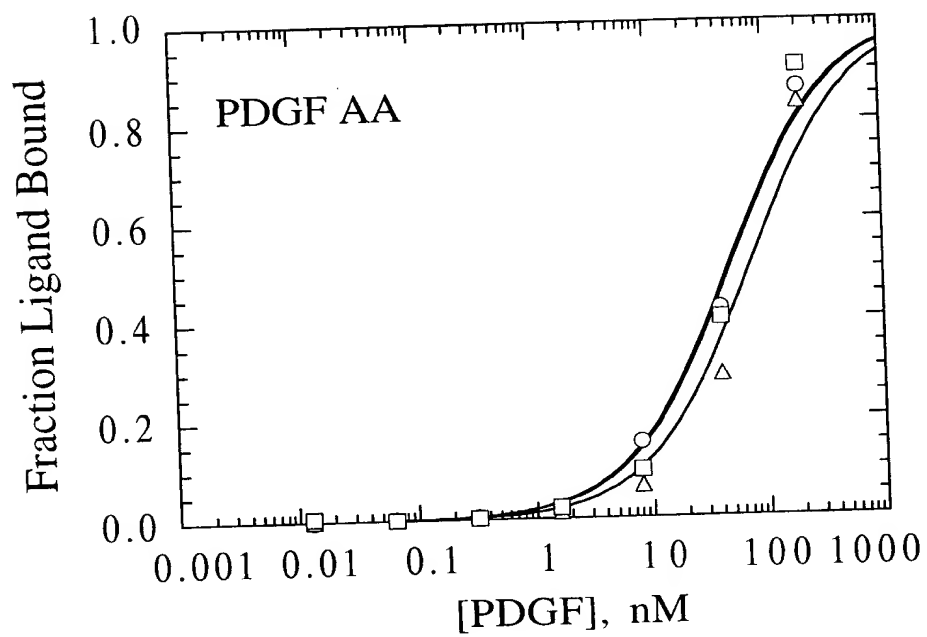


Figure 5A

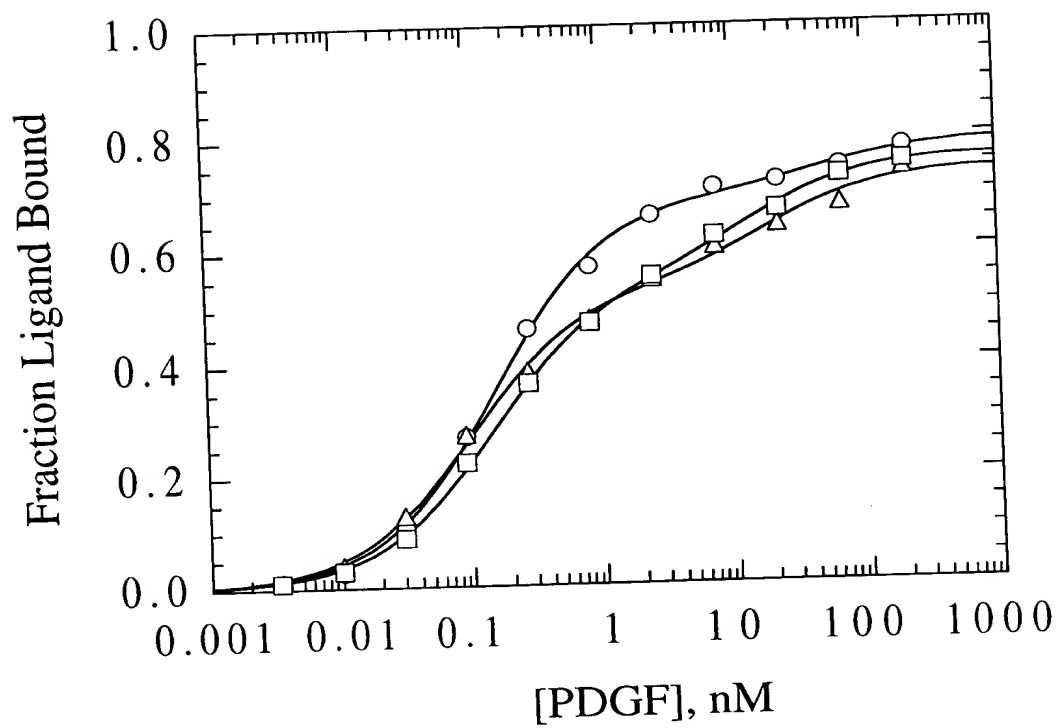


Figure 5B

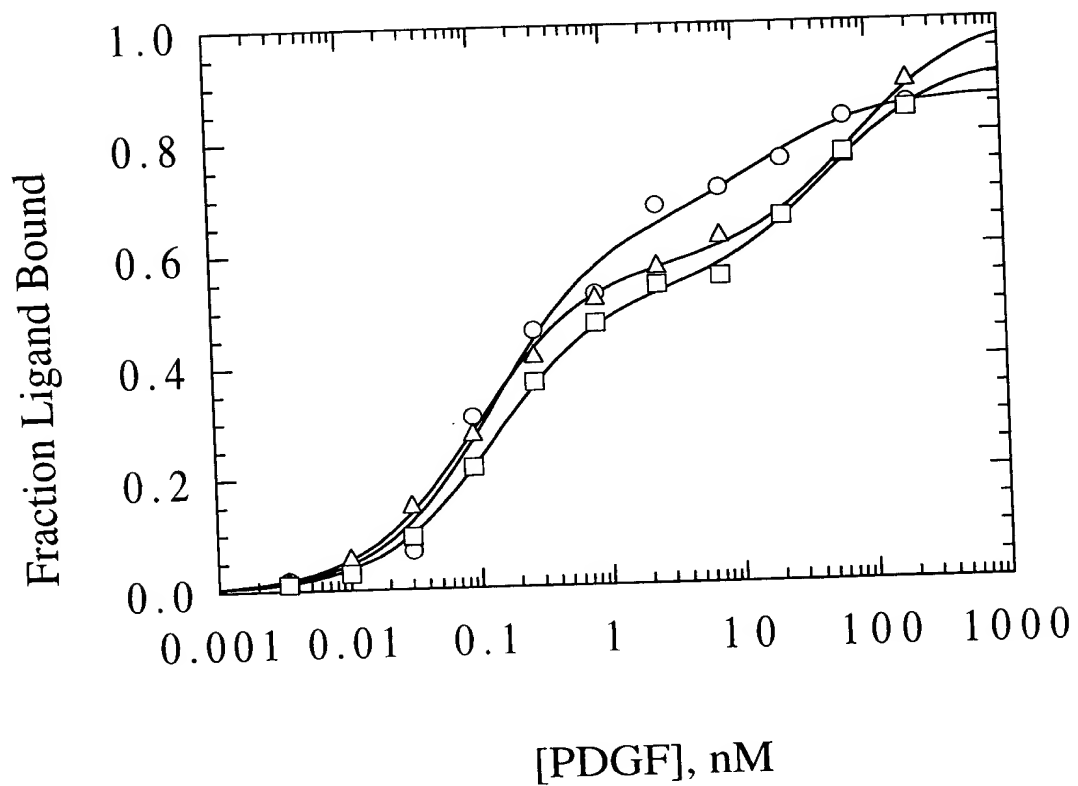


Figure 5C

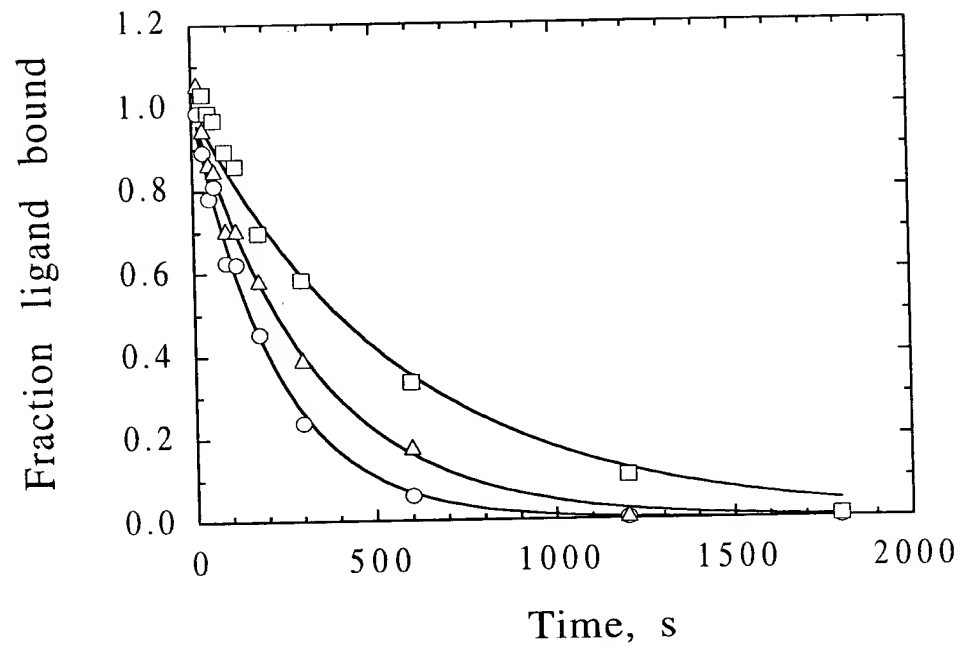


FIGURE 6

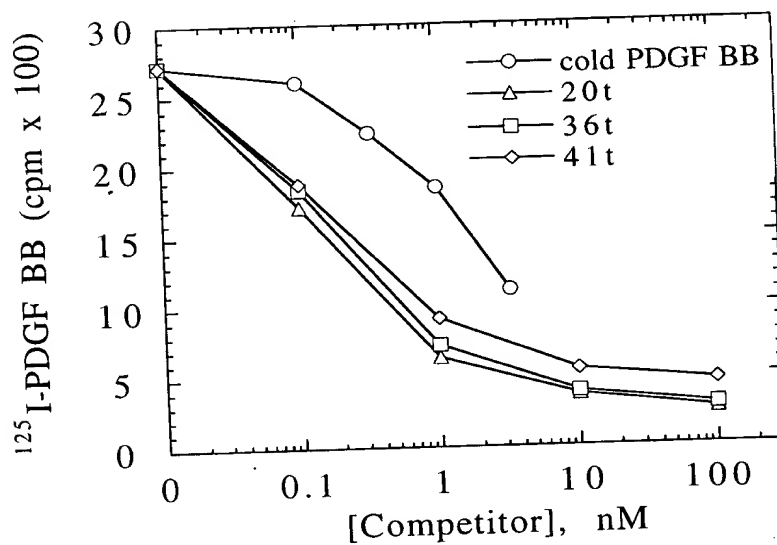


FIGURE 7

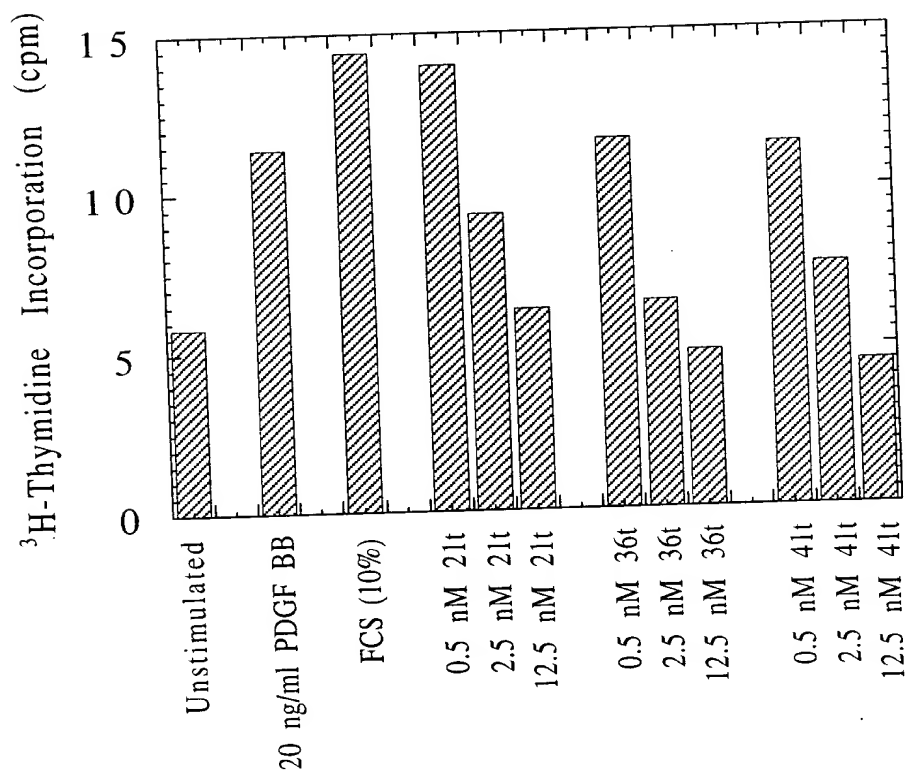
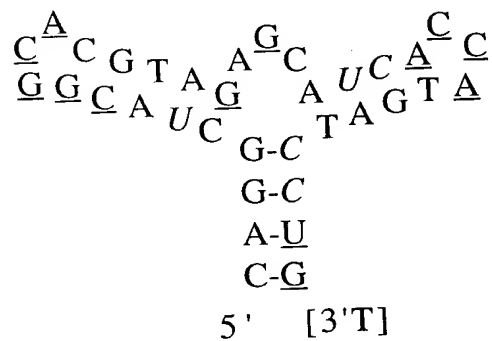
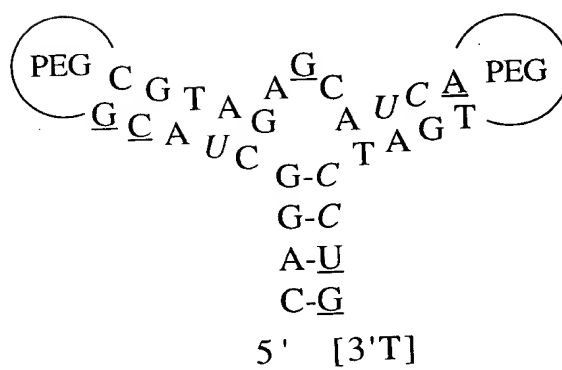


FIGURE 8



$K_d=0.065$ nM

SEQ ID NO: 175



$K_d=0.097$ nM

SEQ ID NO: 176

FIGURE 9

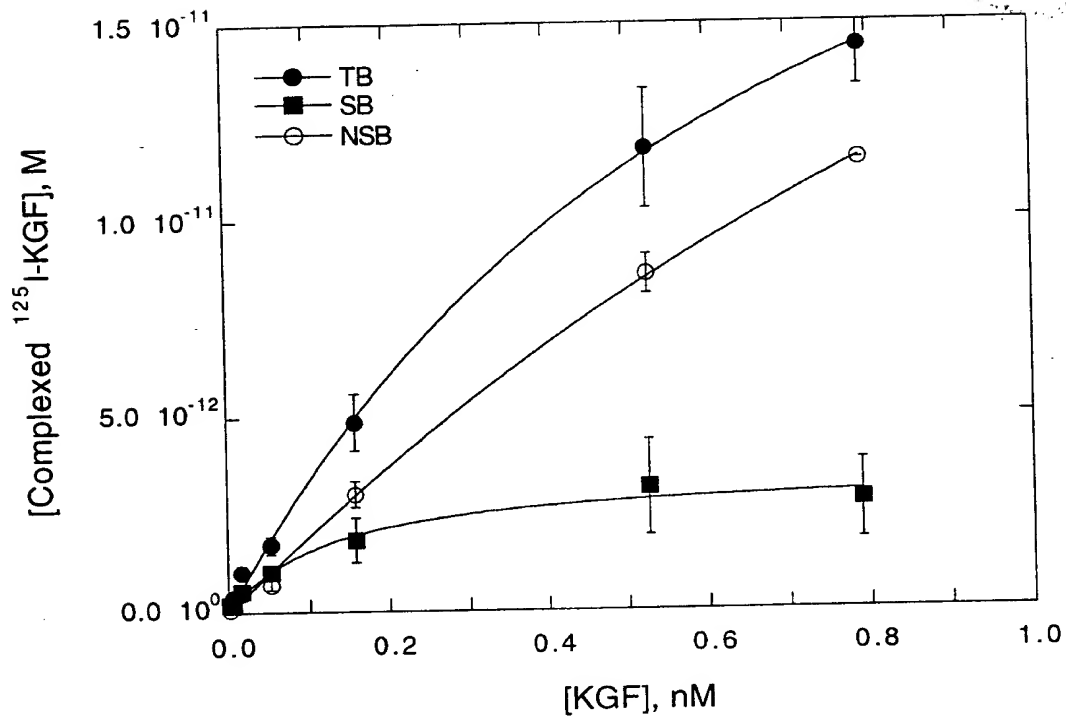


FIGURE 10A

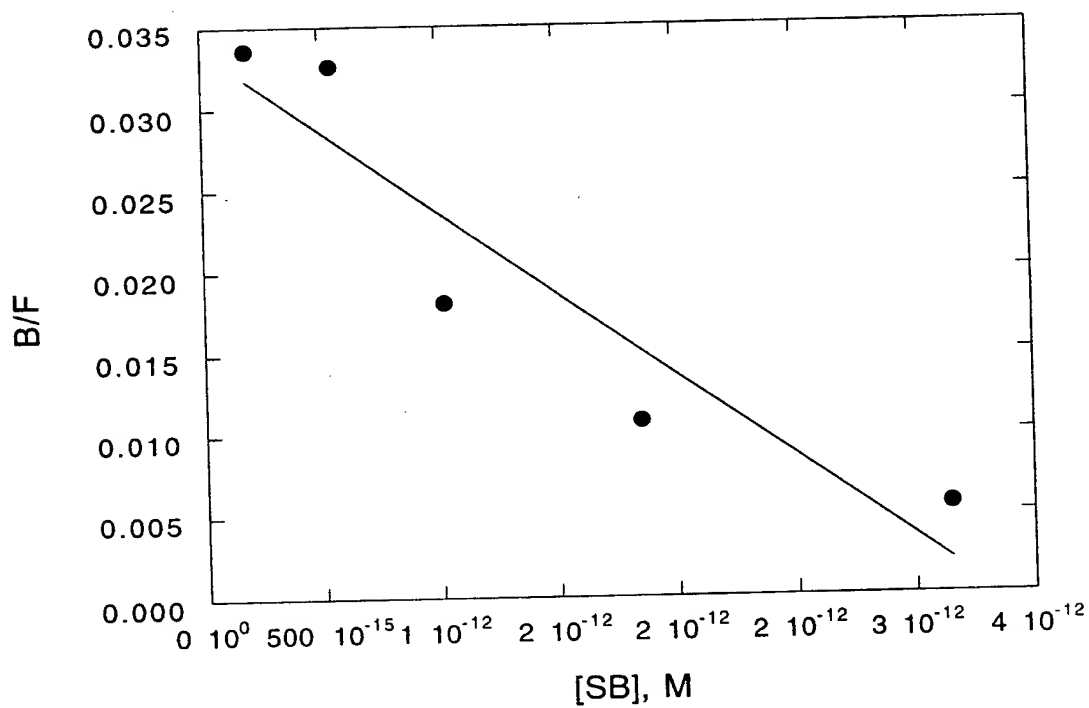


FIGURE 10B

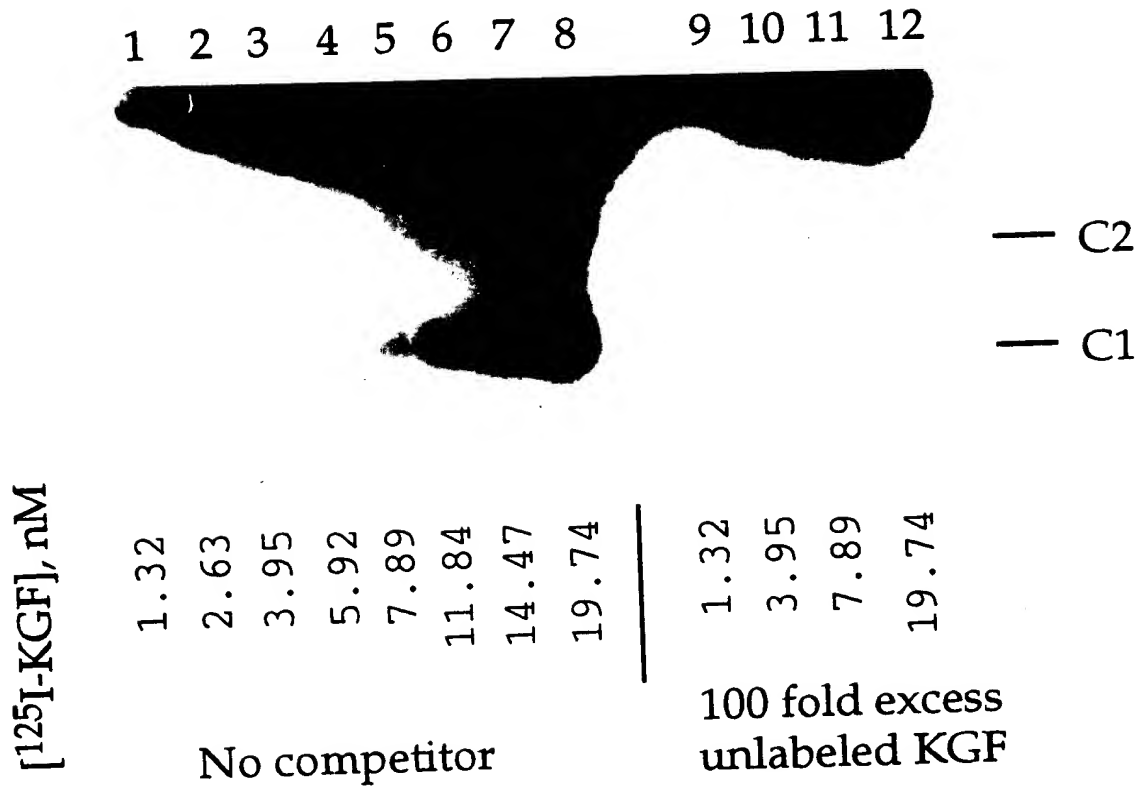


FIGURE 11



Class 1

SEQ ID

Kd, nM

Ki, nM

Clone

NO:

231

232

233

234

235

236

237

238

239

240

241

242

243

244

245

246

247

248

249

250

251

252

253

254

255

256

257

258

259

260

261

262

263

264

265

266

267

268

269

270

271

272

273

274

275

276

277

278

279

280

281

282

283

284

285

286

287

288

289

290

291

292

293

294

295

296

297

298

299

300

301

302

303

304

305

306

307

308

309

310

311

312

313

314

315

316

317

318

319

320

321

322

323

324

325

326

327

328

329

330

331

332

333

334

335

336

337

338

339

340

341

342

343

344

345

346

347

348

349

350

351

352

353

354

355

356

357

358

359

360

361

362

363

364

365

366

367

368

369

370

371

372

373

374

375

376

377

378

379

380

381

382

383

384

385

386

387

388

389

390

391

392

393

394

395

396

397

398

399

400

401

402

403

404

405

406

407

408

409

410

411

412

413

414

415

416

417

418

419

420

421

422

423

424

425

426

427

428

429

430

431

432

433

434

435

436

437

438

439

440

441

442

443

444

445

446

447

448

449

450

451

452

453

454

455

456

457

458

459

460

461

462

463

464

465

466

467

468

469

470

471

472

473

474

475

476

477

478

479

480

481

482

483

484

485

486

487

488

489

490

491

492

493

494

495

496

497

498

499

500

501

502

503

504

505

506

507

508

509

510

511

512

513

514

515

Class 1

 $K_d, K_i,$

Summary Structure



FIGURE 12C

Class 2

SEQ ID NO:	Clone	K _d , nM	K _i , nM
209	47N	1.8	
198	24N	1.2	
202	29N	0.43	13.3
204	35N	2.3	
192	6N	0.7	26.7
190	2N	0.8	66.7
211	54N	5.3	
271			Consensus

AGGAAGGUCAAGAGGAAA CAGC
 gacgaugcgg GUGGGAAGA UGAG
 AGAAGAAUGCA GGAACAGCGAAA
 ugcgggCUUAG GAAA UGGUU
 acgaugcggGC AGGGAGCAA UGAACUCAAGUCAAGCCGUGCACGU | GGGC
 GCGGA AAGGAA CGAGA gggaggacgaugcggGCGGGAAGGUC
 GGG GGAAG GAUU UUGCCcagacgacucgccccga
 CGAA GACC |
 AGCCCCCUGGUGGU |
 Ygay

Summary Structure

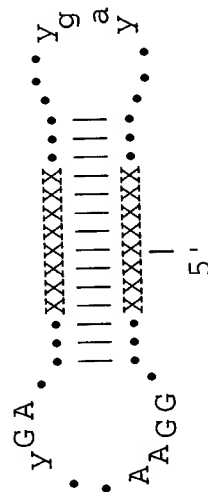


FIGURE 12D

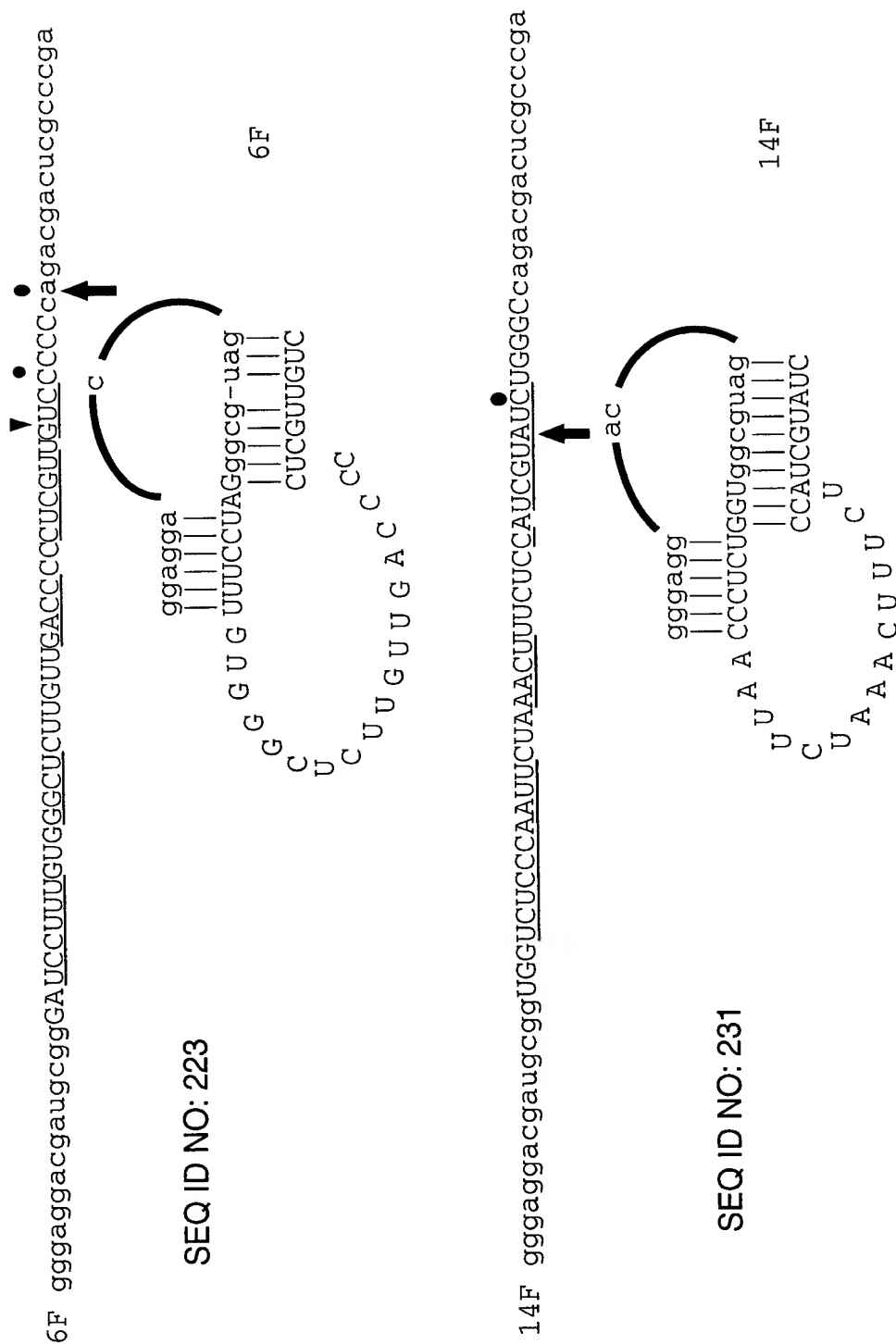


FIGURE 13